Amendments to the Claims

Please cancel Claims 32 and 33. Please amend Claims 2-31 and 35-39. Please add new Claims 40-46. The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

1. (Original) An isolated nucleic acid molecule encoding a protein with a RING-finger domain and 6 NHL-motifs wherein the protein is associated with Lafora's disease.

2. (Currently amended) A nucleic acid according to ~~claim~~ Claim 1 having a sequence ~~as shown in~~ comprising SEQ ID NO:1 ~~(Figure 6A)~~ or SEQ ID NO:3 ~~(Figure 7)~~.

3. (Currently amended) An isolated nucleic acid molecule according to ~~claim~~ Claim 1 comprising

(a) a nucleic acid sequence ~~as shown in~~ comprising SEQ ID NO:1 ~~(Figure 6A)~~ or SEQ ID NO:3 ~~(Figure 7A)~~, wherein T can also be U;

(b) a nucleic acid sequence complementary to (a);

(c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b);

(d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or

(e) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), (b), (c) or (d) under stringent hybridization conditions.

4. (Currently amended) A method of detecting Lafora's disease in a mammal comprising detecting a mutation in a nucleic acid sequence ~~according to any one of claims 1 to 3~~ in a sample from ~~an animal~~ a mammal, wherein said nucleic acid sequence is an isolated nucleic acid molecule encoding a protein with a RING-finger domain and 6 NHL-motifs, and wherein the protein is associated with Lafora's disease.

5. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a C to G change at nucelotide number 205 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

6. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a T to A change at nucleotide number 76 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

7. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotides GA at nucleotide positions 1048 and 1049 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

8. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotides AG at nucleotide positions 468 and 469 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

9. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotide G at nucleotide number 992 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

10. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of 10 bp at nucleotide positions 373 to 382 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

11. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of 32 bp at nucleotide positions 661 to 692 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

12. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a T to C change at nucleotide number 260 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

13. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a A to C change at nucleotide number 905 in the EPM2B gene sequence ~~shown in~~comprising SEQ ID NO:1.

14. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a T to C change at nucleotide number 98 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

15. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting an insert of 2 Ts at nucleotide number 892 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

16. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a G to A change at nucleotide number 436 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

17. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotide T at nucleotide number 1100 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

18. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotide T at nucleotide position 606 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

19. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a A to T change at nucleotide number 923 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

20. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a G to T change at nucleotide number 580 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

21. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a G to T change at nucleotide number 199 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

22. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a G to A change at nucleotide number 838 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

23. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a C to T change at nucleotide number 676 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

24. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotide A at nucleotide position 468 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

25. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a deletion of nucleotide C at nucleotide position 204 in the EPM2B gene sequence ~~shown in~~ comprising SEQ ID NO:1.

26. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting one or more mutations in the EPM2B gene as indicated in Table 1.

27. (Currently amended) A method according to ~~claim~~ Claim 4 comprising detecting a repeat of the sequence GCCGCCCCCCGC (SEQ ID NO:5) at nucleotide position 1001 in the canine sequence of EPM2B ~~shown in~~ comprising SEQ ID NO:3.

28. (Currently amended) A method according to ~~claim~~ Claim 22 comprising detecting at least 3 repeats of SEQ ID NO:5.

29. (Currently amended) A method according to ~~claim~~ Claim 22 comprising detecting at least 10 repeats of SEQ ID NO:5.

30. (Currently amended) A method according to ~~claim~~ Claim 22 comprising detecting from about 14 to about 26 repeats of SEQ ID NO:5.

31. (Currently amended) A method according to ~~any one of claim[s] 4-26~~ Claim 4 wherein the ~~animal~~ mammal is human.

32. (Canceled)

33. (Canceled)

34. (Original) An isolated protein containing a RING-finger domain and six NHL domains which protein is associated with Lafora's disease.

35. (Currently amended) A protein according to ~~claim~~ Claim 34 having the amino acid sequence ~~as shown in~~ comprising SEQ ID NO:2 ~~(Figure 6B)~~ or SEQ ID NO:4 ~~(Figure 7)~~.

36. (Currently amended) A method for detecting Lafora's disease comprising detecting a mutation in a protein according to ~~any one of claims 34 or 35~~ Claim 34.

37. (Currently amended) A method according to ~~claim~~ Claim 36 comprising detecting a mutation in the EPM2B protein as indicated in Table 1.

38. (Currently amended) A kit for carrying out the method of ~~any one of claim s 4 to 33 or 37~~ Claim 4 comprising reagents for the detection of a mutation in a nucleic acid sequence ~~as shown in~~ comprising SEQ ID NO:1 or SEQ ID NO:3.

39. (Currently amended) A kit for carrying out the method of ~~any one of claims 36 or 37~~ Claim 36 comprising reagents for the detection of a mutation in a protein sequence ~~as shown in~~ comprising SEQ ID NO:2 or SEQ ID NO:5.

40. (New) A method of detecting the presence or absence of Lafora's disease in a mammal comprising detecting a mutation in the nucleic acid sequence of Claim 1 wherein the nucleic acid sequence comprises SEQ ID NO:1 or SEQ ID NO:3.

41. (New) A method of detecting the presence or absence of Lafora's disease in a mammal comprising detecting a mutation in the nucleic acid sequence of Claim 1 wherein the nucleic acid sequence comprises:

(a) a nucleic acid sequence comprising SEQ ID NO:1 or SEQ ID NO:3, wherein T can also be U;

(b) a nucleic acid sequence complementary to (a);

(c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b);

(d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or

(e) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), (b), (c) or (d) under stringent hybridization conditions.

42. (New) A method for detecting the presence or absence of Lafora's disease comprising detecting a mutation in a protein according to claim 35.

43. (New) A method of detecting the presence of absence of a mutation in the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3 comprising the steps of:

(a) analyzing a test sample containing the EPM2B gene to determine the nucleic acid sequence of the gene;

(b) comparing the nucleic acid sequence of the gene in the test sample to the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3; and

(c) determining the differences, if any, between the sequence of the EPM2B gene in the test sample and the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:3, thereby detecting the presence of absence of a mutation in the nucleotide sequence set forth in SEQ ID NO:1 or SEQ ID NO:3 in a mammal.

44. (New) A method for diagnosing the presence of, or predisposition to, Lafora's disease in a mammal comprising:

(a) obtaining a nucleic acid sample from the mammal;

(b) analyzing the nucleic acid sample to determine the presence of absence of a EPM2B gene mutation associated with Lafora's disease, wherein the presence of an EPM2B

gene mutation associated with Lafora's disease indicates that the mammal is at risk for development of Lafora's disease.

45. (New) A method according to Claim 4 wherein the mutation is a deletion, insertion, point mutation, or repeat sequence.

46. (New) A method according to Claim 44 wherein the mutation is a deletion, insertion, point mutation, or repeat sequence.